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Supporting Information

The following supporting information is available for this article:

Figure S1. Phylogenetic trees inferred by maximum likelihood with a forced molecular clock for: (A) the three-locus tree (multilocus3), (B) the seven-locus tree (multilocus7), and (C) the chromosome tree (chromosome).

Figure S2. Phylogenetic tree inferred by Bayesian Estimation of Species Trees (BEST).

Figure S3. For most of the seven individual locus phylogenies trees, likelihood ratio tests indicate that the pure-birth model with decaying diversification rate is significantly more likely than a pure-birth model with constant rate regardless of the assumed number of species in the *B. burgdorferi* sl clade.

Supporting Information may be found in the online version of this article.

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